

# Computational Chemistry Beyond Petascale

Jeff Hammond

Argonne Leadership Computing Facility

10 November 2010



# Background

- 2009-present — Argonne Director's Fellowship
- Summer 2006 — NWChem internship
- 2005-2009 — DOE-CSGF
- 2003-2009 — UChicago Chemistry



THE UNIVERSITY OF  
CHICAGO



**NWCHEM**

HIGH-PERFORMANCE COMPUTATIONAL  
CHEMISTRY SOFTWARE

# Outline

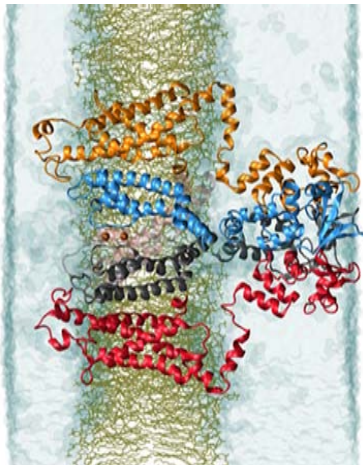
- 1 Brief overview of computational chemistry
- 2 Why exascale matters to chemists
- 3 Four examples of massive parallelism transforming chemical applications

# Computational chemistry

# Atomistic simulation in chemistry

- 1** classical molecular dynamics (MD) with empirical potentials
- 2** ab initio molecular dynamics based upon density-function theory (DFT)
- 3** quantum chemistry with wavefunctions  
e.g. coupled-cluster (CC)

# Classical molecular dynamics



- Solves Newton's equations of motion with empirical terms and classical electrostatics.
- Size: 100K-10M atoms
- Time: 1-10 ns/day
- Scaling:  $\sim N_{atoms}$

Data from K. Schulten, et al. "Biomolecular modeling in the era of petascale computing." In D. Bader, ed., *Petascale Computing: Algorithms and Applications*.

Image courtesy of Benoît Roux via ALCF.

# Car-Parrinello molecular dynamics

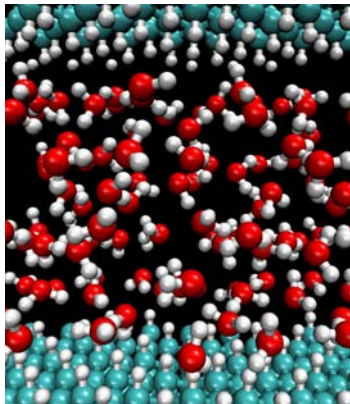
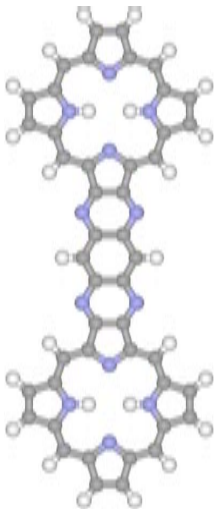


Image courtesy of Giulia Galli via ALCF.

- Forces obtained from solving an approximate single-particle Schrödinger equation; time-propagation via Lagrangian approach.
- Size: 100-1000 atoms
- Time: 0.01-1 ns/day
- Scaling:  $\sim N_{el}^x$  ( $x=1-3$ )

F. Gygi, *IBM J. Res. Dev.* **52**, 137 (2008); E. J. Bylaska et al. *J. Phys.: Conf. Ser.* **180**, 012028 (2009).

# Coupled-cluster theory



- Infinite-order solution to many-body Schrödinger equation truncated via clusters.
- Size: 10-100 atoms
- Time: N/A
- Scaling:  $\sim N_{bf}^x$  ( $x=4-7$ )

Image courtesy of Karol Kowalski and Niri Govind.



# Chemistry on supercomputers

Both classical and ab initio molecular dynamics have essentially reached algorithmic maturity. Most research is fighting Amdahl's law and related concepts (FFT does not scale), e.g. DEShaw has turned classical molecular dynamics into an engineering problem.

Quantum many-body methods are far from algorithmic maturity because they have been constrained to tiny systems so the N-body problem is hidden behind dense linear algebra.

Dense linear algebra is great for Gordon Bell Prizes but terrible for science.

# Why is exascale different *for chemists?*



## Is this exciting? Yes!

- s **Solution of longstanding problems**
  - Detailed chemical reaction dynamics in solution
  - Molecular level environmental chemistry
  - Ab initio design of catalysts
  - Ab initio molecular dynamics

- s **New “Grand Challenges”**

- s **Computational chemistry as a design tool**

- Interactive, quantitative response to posed questions
- Will the real impact of petaflop computing be that you can have all the tflop computing you need without waiting? On your desk?

# Why is computational chemistry different?

- Community doesn't care unless they can afford hundreds of jobs *per chemist*.
- We cannot discriminate between the **thousands** of important questions which can be answered by computation.
- The impact of hero simulations is often psychological (moving the flag).

# Why is exascale different for chemists?

Exascale is different for chemists because of what happens at petascale.

Petascale is the crossover point between algorithmic approaches for quantum chemistry many-body methods wherein the scalable sparse algorithms overtake the canonical dense algorithms.

Quantum nearsightedness doesn't help if the world is only three inches around!

Even without nearsightedness, massive parallelism opens doors into totally new application areas.

# Electronic excited-states in biology

Joint work with Benoît Roux (UC/ANL) and Karol Kowalski (PNNL).

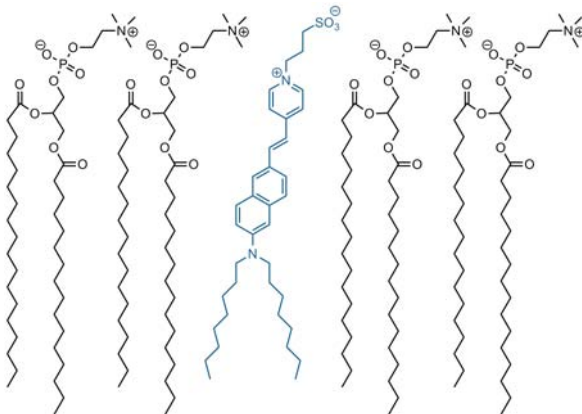
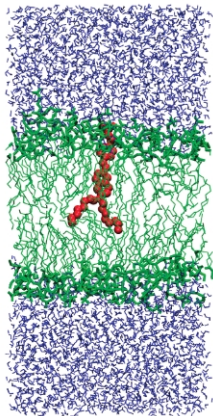
# Molecular probes

*Optical potentiometric probes have become important tools in electrophysiology. These organic molecules display spectroscopic responses to membrane potential and have been used for the study and characterization of model membranes, nerve and muscle tissues, organelles, microorganisms, and red blood cells. They can often be used in place of conventional microelectrodes and lend themselves to many system not accessible to microelectrodes.*

E. Fluhler, V. G. Burnham, L. M. Loew, *Biochemistry* **24** , 5749 (1985). "Spectra, membrane binding, and potentiometric responses of new charge shift probes."



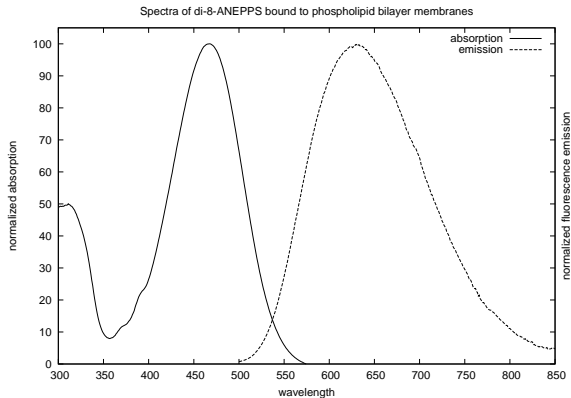
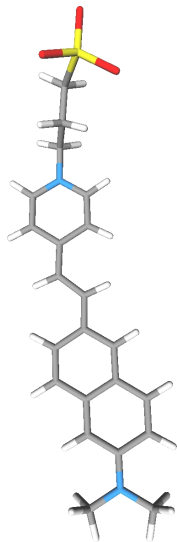
# Membrane configuration of di-8-ANEPPS



C. F. Rusu, H. Lanig, O. G. Othersen, C. Kryschi, and T. Clark, *J. Phys. Chem. B* **112**, 2445 (2008).

# ANEPPS model structure

peaks = 2.655 eV (3.987 eV) and 1.965 eV



<http://probes.invitrogen.com/media/spectra/data/3167lip.txt>

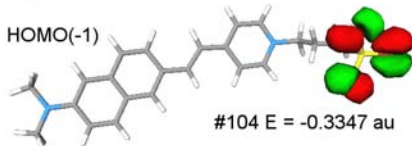
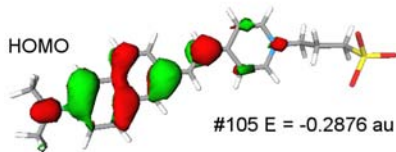
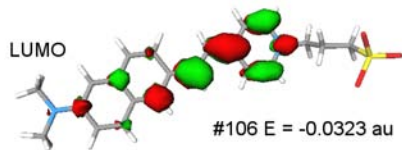
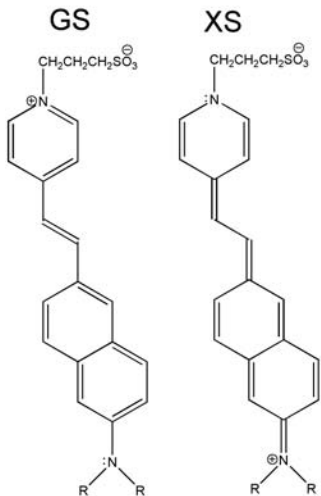
# Computing the spectrum

## Method comparison

Root	au	eV	nm	OS
B3LYP/cc-pVDZ	0.002	0.06	19758.1	0.001
B3LYP/aug-cc-pVDZ	0.016	0.44	2799.2	0.000
PBE0/aug-cc-pVDZ	0.026	0.70	1773.5	0.000
BH&H/aug-cc-pVDZ	0.091	2.47	501.7	0.000
TDHF/aug-cc-pVDZ	0.124	3.38	366.7	1.731
CIS/aug-cc-pVDZ	0.132	3.59	345.8	1.949

The basis set dependence is an illusion.

# What are the electrons doing?



# Computing the spectrum

## Many-body methods

Basis	$\tau$	eV	au	nm
CC2/6-31G*	1.5	1.815	0.067	683.3
	0.5	3.629	0.133	341.6
	0.7	3.231	0.119	383.8
CCSD/6-31G*	1.5	2.984	0.110	415.5
	2.0	2.962	0.109	418.6
	$\infty$	2.968	0.109	417.7
CCSD/cc-pVDZ	$\infty$	2.945	0.108	421.0
Experiment		2.655	0.098	467

# Accurate many-body methods

## CR-EOM-CCSD(T) excitation energies

Method	Basis	$\tau$	eV	au	nm
EOM-CCSD	6-31G*	0.5	3.629	0.133	341.6
	6-31G*	0.7	3.231	0.119	383.8
	6-31G*	1.5	2.980	0.110	416.1
CR-EOM-CCSD(T)	6-31G*	0.5	3.590	0.132	345.4
	6-31G*	0.7	3.150	0.116	393.6
	6-31G*	1.5	2.810	0.103	441.2
Experiment			2.655	0.098	467

# NWChem implementation (TCE)

## Timings on 256 nodes of Chinook

Procedure	wall time (s)
SCF total time	57
four-index transformation	192
<b>one</b> CCSD iteration	157
<b>one</b> EOM-CCSD iteration	252
CR-EOM-CCSD(T) evaluation	6301
Total time	12510

Even though this calculation is trivial with NWChem, it is still impossible with single-node codes because of the memory wall.

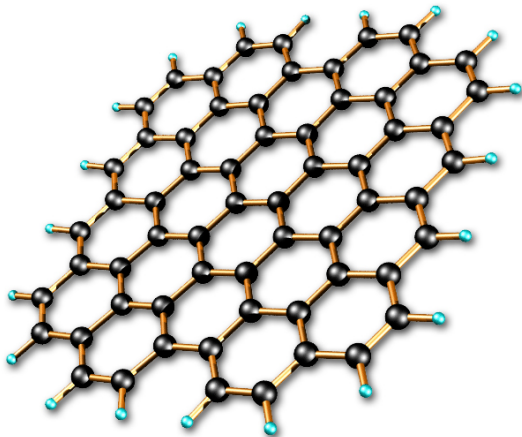
Karol is up to 25K cores at NERSC...

# Bottom-up simulation in material science

Joint work with Karol Kowalski (PNNL).



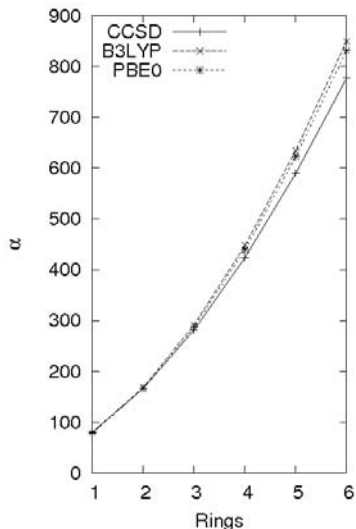
# Graphitic materials



Polarizability  
simultaneously  
probes excited-state  
behavior (poles)  
and intermolecular  
forces — dispersion  
closely related to  
 $\alpha(\omega)$ .

Image from Berkeley Labs (Lanzara Group).

# Polarizabilities of polyacenes



In June 2006, benzene (1 ring) was the largest CCSD-LR  $\alpha(\omega)$  calculation ever performed.

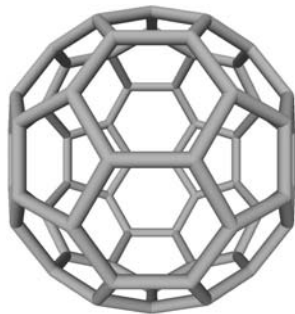
Rings	$\alpha_{LL}$		
	CCSD	B3LYP	PBE0
1	80.57	79.38	78.75
2	166.61	168.59	166.48
3	281.60	291.56	287.07
4	423.83	447.60	439.52
5	589.97	634.65	622.40
6	776.83	849.55	831.79

*J. Chem. Phys.* **127**, 144105 (2007).

# Polarizabilities of C<sub>60</sub>

## Theory versus experiment

Method	Wavelength (nm)	
	$\infty$	1064
Lowest found	441.3	-
B3LYP/6-31G*	469.0	-
HF/6-31++G	506.8	515.6
<b>Experiment</b>	516.3	533.1
CCSD/Z3Pol	555.3	564.9
LDA/TZP++	571.6	-
CC2/6-31++G	586.8	600.8
CC2/6-31++G*	606.8	622.6
CC2/aug-cc-pVDZ	623.7	640.2
Highest found	1033.2	-



*J. Chem. Phys.* **129**, 226101 (2008).

# Moving the flag

## What happened?

Applying CCSD to  $C_{60}$ ...

... was laughable in 2000.

... was impossible in 2005.

... was heroic in 2007.

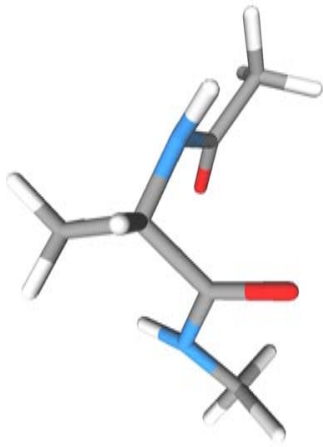
... is mundane in 2010.

- automatic code generation was critical in implementing CCSD-LR in parallel
- finally had a machine that could hold everything in memory
- enough resources such that an intern wasn't afraid to burn millions of hours a year

# Force-fields from first-principles

Joint work with Karl Freed (UC), Benoît Roux (UC/ANL), Alex MacKerell (Maryland)

# The protein prototype — dialanine



- Debatable if dialanine represents the real torsional potential.
- Many FF potentials use MP2 dialanine results.
- Useful for calibrating methods without pollution of cooperative effects.
- Computationally tractable for CCSD(T) (whole  $\phi$ - $\psi$  map).

# Evaluating models with CCSD(T)

Method	MUE	Max	Method	MUE	Max
MP2	0.436	1.304	M05	1.551	8.389
CCSD	0.577	1.426	TPSS+D	1.593	9.258
B2PLYP	0.913	4.690	FT97	1.711	11.047
M06	1.137	4.874	CAMB3LYP	1.747	6.268
Becke97+D	1.177	5.981	M06-2X	1.757	5.812
Becke98	1.287	7.526	BB1K	1.773	7.310
TPSS	1.312	10.691	B2LYP	1.913	6.514
B3LYP+D	1.327	6.379	HCTH120	2.119	10.141
TPSSh	1.330	9.525	BOP	2.614	9.118
M06-L	1.378	6.657	M06-HF	2.884	12.286
Becke97	1.391	7.486	SCF	3.066	11.076
PBE+D	1.404	9.812	HCTH407	3.168	9.678
X3LYP	1.430	7.747	HCTH	3.330	9.788
B3LYP	1.456	7.884	CAMPBE0	3.348	10.676
PBE0	1.506	8.041			

# Evaluating models with CCSD(T)

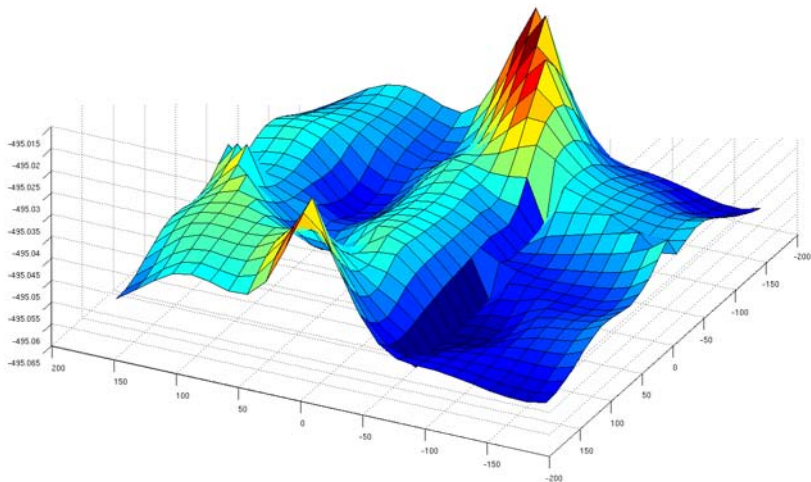
## Observations

- Justified using MP2 for fitting torsional parameters.
- Approximate functionals are getting better with time.
- DFT+D improves results in most cases.
- Unlikely that a density functional better than MP2 exists.
- CCSD(T) takes approximately 1 hour per job on 64 nodes.



# Endgame for dialanine

CCSD(T)/cc-pVTZ energies at MP2/cc-pVTZ geometries.



# Beyond petroleum for the chemical industry

Joint work with Larry Curtiss (ANL) and Jeff Greeley (ANL).

# Chemistry after oil

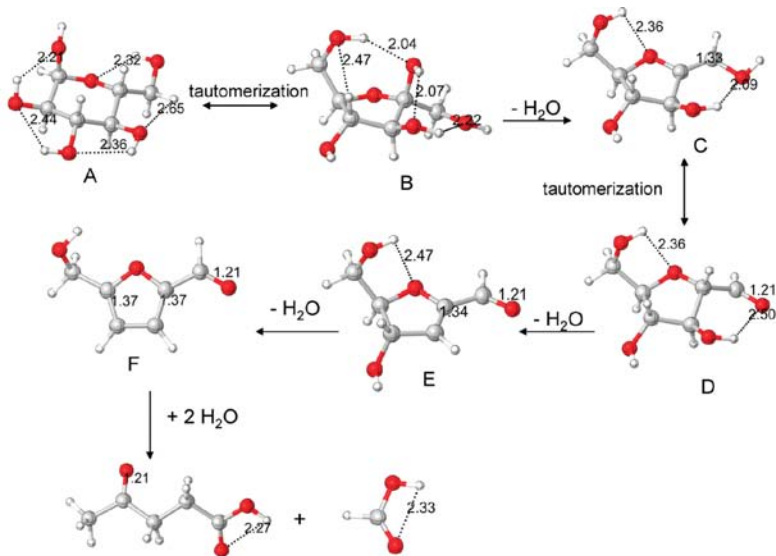
Oil won't disappear, but the price is going to go way up.

Cannot live without plastic and cannot pay more for commodities.

Levulinic acid is a precursor for polymers, plastics and pharmaceuticals.

If we can convert cheap, abundant, non-petroleum chemicals into levulinic acid, there is potential for a chemical industry after oil.

# From glucose to levulinic acid



# Computational details

The CCSD(T) calculations in the G4 method were prohibitively slow (weeks) using Gaussian, but ran in less than one hour on 1024 nodes of Blue Gene/P using NWChem.

We optimized NWChem CCSD(T) code for Blue Gene/P by developing the first threaded kernels and improving ARMCI.

Larry's G3/G4 methods are the standard model for thermochemistry. If they run on supercomputers rather than workstations, the possible applications grow exponentially.

# Summary

Supercomputers and parallel software were critical to the accurate study of four systems:

- 1 di-8-ANEPPS ion channel probe
- 2 C<sub>60</sub> and graphic materials
- 3 dialanine protein model
- 4 glucose to levulinic acid

Exascale means the democratization of such capability as well as a paradigm shift in quantum many-body algorithms.

The **Chemistry Exascale Codesign Center** will deliver the transformative software capability required to realize the potential of accurate simulations in many critical areas (biology, material science, energy science).

# Extras

# Density-functional theory

$$E = T[\rho] + U[\rho] + V_{XC}[\rho]$$

which are the kinetic, Coulomb and exchange-correlation components. In practice,  $\rho \leftarrow \{\phi_i\}$  so  $T[\rho] = T[\{\phi_i\}]$ .

Category	Functional form	Example
LDA	$V_{XC}[\rho_\sigma]$	LDA
GGA	$V_{XC}[\rho_\sigma, \nabla\rho_\sigma]$	BLYP, PBE
Hybrid GGA	$\alpha V_{XC}[\rho_\sigma, \nabla\rho_\sigma] + \beta V_X[\{\phi_i\}]$	B3LYP, PBE0
Meta GGA	$V_{XC}[\rho_\sigma, \nabla\rho_\sigma, \tau_\sigma]$	TPSS
Double-hybrid	$V_{XC}[\rho_\sigma, \nabla\rho_\sigma, \vec{\epsilon}_\sigma]$	B2PLYP

The exact functional form is not known. The coefficients are usually fit to data but occasionally determined from first-principles.



# Coupled-cluster theory

$$\begin{aligned} |CC\rangle &= \exp(T)|0\rangle \\ T &= T_1 + T_2 + \cdots + T_n \quad (n \ll N) \\ T_1 &= \sum_{ov} t_o^v \hat{a}_v^\dagger \hat{a}_o \end{aligned}$$

- Can do excited-states and arbitrary-order properties
- Fast convergence in  $T$  — singles and doubles (CCSD) are an excellent approximation for many problems
- Perturbative corrections, namely CCSD(T), produce extremely accurate results at  $n_{iter} N^6 + N^7$  cost ( $n_{iter} \approx 20$ ).
- Memory-bound but highly parallelizable.

# Evaluating models with CCSD(T)

- Used OPLS-AA geometries to prevent bias.
- 6-311++G\*\* basis set (aug-cc-pVTZ desirable).
- Difference between 6-31+G\* and 6-311++G\*\*:  
SCF=1.18, MP2=2.48 (MUE in kJ/mol).
- Difference between 6-311++G\*\* and aug-cc-pVTZ:  
SCF=0.89, MP2=1.70 (MUE in kJ/mol).
- 350 configurations (30° grid everywhere, 10° in basins).